

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1900	100.0		370	2	JC2443	chemokine (C-C) re
2	1651.5	86.9		374	2	I38450	chemokine (C-C) re
3	1564	71.8		352	2	A43113	chemokine (C-C) re
4	1036	54.5		355	2	A45177	chemokine (C-C) re
5	1010.5	53.2		359	2	I49341	MIP-1 alpha recept
6	963.5	50.7		355	2	I49339	macrophage inflamm
7	951	50.1		355	2	G02436	chemokine (C-C) re
8	871	45.8		360	2	JC4587	chemokine (C-C) re
9	862.5	45.4		360	2	A57160	chemokine (C-C) re
10	822.5	43.3		383	2	S55594	G protein-coupled
11	778.5	41.0		356	2	I49340	MIP-1 alpha recept
12	751	39.5		355	2	JC5067	G protein-coupled
13	722.5	38.0		354	2	I38186	probable G protein
14	708	37.3		355	2	JC4304	orphan G protein-c
15	649.5	34.2		344	2	JC5942	chemokine receptor
16	581.5	30.6		378	2	B55735	lymphocyte-specifi
17	569	29.9		378	2	A55735	G protein-coupled
18	567.5	29.6		378	2	A45680	G protein-coupled
19	563	29.6		369	2	JC5068	G protein-coupled
20	547	28.8		360	2	A53611	interleukin-8 rece
21	540.5	28.4		355	2	JQ1231	interleukin-8 rece
22	540.5	28.4		359	2	A48921	interleukin-8 rece
23	536.5	28.2		358	2	A53752	interleukin-8 rece
24	532.5	28.0		356	2	A42096	interleukin-8 rece
25	532	28.0		367	2	JF0349	interferon-inducib
26	528.5	27.8		333	2	I65989	G protein-coupled
27	528.5	27.8		350	2	A39445	interleukin-8 rece
28	515.5	27.1		352	2	G00048	fusin (LESTRA) - c
29	515	27.1		353	2	S28787	neuropeptide Y/pep

Db 61 MLVVLILINCKKLL

61 MLVVLILINCKKLCTDIYLLNLAISDLLFLITLPLWAHSAANEWFVFGNAMCKLF

QY 121 HIGYEGGIFFIILLIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
Db 121 HIGYEGGIFFIILLIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
QY 181 COKEDSVVCGPYFPRGWNFFTHIRNIIIGLVLPPLIMVICYGIILKTLRCRNEKKRRH 240  
Db 181 COKEDSVVCGPYFPRGWNFFTHIRNIIIGLVLPPLIMVICYGIILKTLRCRNEKKRRH 240  
QY 241 AVRVIITIMVYFLEWTPYPIVILLNTFOEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
Db 241 AVRVIITIMVYFLEWTPYPIVILLNTFOEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
QY 301 NPIIYAFVGEKFRYLSVFFRKHIKRFCKQCPVFYRETVDGVTSTNTSTGQEVSAAGL 360  
Db 301 NPIIYAFVGEKFRYLSVFFRKHIKRFCKQCPVFYRETVDGVTSTNTSTGQEVSAAGL 360

RESULT 2  
138450  
chemokine (C-C) receptor 2, splice form A - human  
N:Alternate names: C-C CKR-2; monocyte chemoattractant protein 1 receptor; monocyte chemokine (C-C) receptor 5 - human  
C:Species: Homo sapiens (man)  
C:Date: 16-Feb-1996 #sequence\_revision 16-Feb-1996 #text\_change 13-Aug-1999  
C:Accession: U38450  
R:Charo, I.F.; Myers, S.J.; Herman, A.; Francis, C.; Connolly, A.J.; Coughlin, S.R.  
Proc. Natl. Acad. Sci. U.S.A. 91, 2752-2756, 1994  
A:Title: Molecular cloning and functional expression of two monocyte chemoattractant proteins 1 and 2  
A:Reference number: A53477; MUID:94195821; PMID:8146186  
A:Accession: U38450  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <RES>  
A:Cross-references: EMBL:U03882; NID:9472555; PIDN:AAA19119.1; PID:g472556  
C:Genetics:  
A:Gene: GDB:CMKBR2  
A:Cross-references: GDB:337364; OMIM:601267  
A:Map position: 3p21-3p21  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: alternative splicing; G protein-coupled receptor; glycoprotein; transmembrane protein  
F:44-68/Domain: transmembrane #status predicted <TM1>  
F:79-99/Domain: transmembrane #status predicted <TM2>  
F:115-136/Domain: transmembrane #status predicted <TM3>  
F:154-178/Domain: transmembrane #status predicted <TM4>  
F:208-226/Domain: transmembrane #status predicted <TM5>  
F:244-265/Domain: transmembrane #status predicted <TM6>  
F:292-309/Domain: transmembrane #status predicted <TM7>  
F:14/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:32-277,113-190/Disulfide bonds: #status predicted

Query Match 86.9%; Score 1651.5; DB 2; Length 374;  
Best Local Similarity 95.5%; Pred. No. 5.9e-133;  
Matches 319; Conservative 3; Mismatches 5; Indels 7; Gaps 3;

QY 1 MLSTSRFRINTNSESGETVTFDDYDYGAPCHKFDVKQIGQALLPPLSLVFIQFVGN 60  
Db 1 MLSTSRFRINTNSESGETVTFDDYDYGAPCHKFDVKQIGQALLPPLSLVFIQFVGN 60  
QY 61 MLVLLILNCKKLCTDIYLLNLALISDLFLITPLWAHSAANWVFGNAMKLFETGLY 120  
Db 61 MLVLLILNCKKLCTDIYLLNLALISDLFLITPLWAHSAANWVFGNAMKLFETGLY 120  
QY 121 HIGYEGGIFFIILLIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
Db 121 HIGYEGGIFFIILLIDRYLAIVHAVFALKARTVTFGVVTSVITWLVAVFASVPGIIFTK 180  
QY 181 COKEDSVVCGPYFPRGWNFFTHIRNIIIGLVLPPLIMVICYGIILKTLRCRNEKKRRH 240  
Db 181 COKEDSVVCGPYFPRGWNFFTHIRNIIIGLVLPPLIMVICYGIILKTLRCRNEKKRRH 240  
QY 241 AVRVIITIMVYFLEWTPYPIVILLNTFOEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300  
Db 241 AVRVIITIMVYFLEWTPYPIVILLNTFOEFFGLSNCESTSQLDQATQVTTGLMTHCCI 300

QY 301 NPIIYAFVGEKFRYLSVFFRKHIKRFCKQCPV 334  
Db 301 NPIIYAFVGEKFRYLSVFFRKHIKRFCKQCPV 334

RESULT 3  
A43113  
chemokine (C-C) receptor 5 - human  
N:Alternate names: C-C CKR-5; CCR5  
C:Species: Homo sapiens (man)  
C:Date: 12-Jul-1996 #sequence\_revision 12-Jul-1996 #text\_change 20-Jun-2000  
C:Accession: A43113; S71808; A58834; A58832; G02653; A58833  
R:Samson, M.; Labbe, O.; Mollereau, C.; Vassart, G.; Parmentier, M.  
Biochemistry 35, 3362-3367, 1996  
A:Title: Molecular cloning and functional expression of a new human CC-chemokine receptor  
A:Reference number: A43113; MUID:96241590; PMID:8639485  
A:Accession: A43113  
A:Molecule type: mRNA  
A:Residues: 1-352 <SAM1>  
A:Cross-references: GB:X91492; NID:gl262810; PIDN:CAA62796.1; PID:gl262811  
R:Samson, M.; Libert, F.; Doranz, B.J.; Rucker, J.; Liesnard, C.; Farber, C.M.; Saragaglia, M.; Inai, T.; Rana, S.; Yi, Y.; Smyth, R.J.; Collman, R.G.; Doms, R.W.; Vassart, G.; Nature 382, 722-725, 1996  
A:Title: Resistance to HIV-1 infection in caucasian individuals bearing mutant alleles of the A-10 polymorphism of the chemokine receptor 5 (CCR5) gene  
A:Reference number: S71808; MUID:96345670; PMID:8751444  
A:Accession: S71808  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 182-206; 207-230 <SAM2>  
A:Accession: A58834  
A:Status: nucleic acid sequence not shown; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-184; 'INDSHLGAGPAAACHGILLGNPKNSASVSK' <SAM3>  
A:Cross-references: GB:X99393; NID:gl524062; PIDN:CAA67767.1; PID:gl524063  
A:Note: this frameshift mutation results in a non-functional receptor but confers a resistance to HIV-1 infection  
R:Combadiere, C.; Ahuja, S.K.; Tiffany, H.L.; Murphy, P.M.; J. Leukoc. Biol. 60, 147-152, 1996  
A:Title: Cloning and functional expression of CC CKR5, a human monocyte CC chemokine receptor  
A:Reference number: A58832; MUID:96295970; PMID:8699119  
A:Accession: A58832  
A:Molecule type: mRNA  
A:Residues: 1-352 <COM1>  
A:Cross-references: GB:U57840; NID:gl502408; PIDN:AAH17071.1; PID:gl502409  
A:Experimental source: clone 8, endotoxin-stimulated peripheral blood monocytes  
R:Combadiere, C.  
Submitted to the EMBL Data Library, May 1996  
A:Reference number: H01541  
A:Accession: G02653  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-89; 'L', '91-352 <COM2>  
A:Cross-references: EMBL:U57840  
R:Raport, C.J.; Gosling, J.; Schweickart, V.L.; Gray, P.W.; Charo, I.F.; J. Biol. Chem. 271, 17161-17166, 1996  
A:Title: Molecular cloning and functional characterization of a novel human CC chemokine receptor  
A:Reference number: A58833; MUID:96291862; PMID:8663314  
A:Accession: A58833  
A:Molecule type: mRNA  
A:Residues: 1-352 <RAP>  
A:Cross-references: GB:U54994; NID:gl457945; PIDN:AAH50598.1; PID:gl457946  
C:Comment: This is a receptor for chemokines MIP-1alpha (see PIR:A30574), MIP-1beta (see PIR:A30574) and dual-tropic strains of HIV-1 bind to a complex of chemokine receptors  
C:Genetics:  
A:Gene: GDB:CMKBR5; CCR5; CKR-5; OMIM:601373  
A:Cross-references: GDB:1230510; OMIM:601373  
A:Map position: 3p21-3p21  
C:Function:  
A:Description: G protein-coupled receptor for chemokines MIP-1alpha, MIP-1beta and RANTES  
A:Note: probably acts to control granulocyte proliferation and differentiation  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: AIDS; G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane protein  
F:32-56/Domain: transmembrane #status predicted <TM1>

F;67-87/Domain: transmembrane #status predicted <TM2>  
F;103-124/Domain: transmembrane #status predicted <TM3>  
F;142-166/Domain: transmembrane #status predicted <TM4>  
F;193-218/Domain: transmembrane #status predicted <TM5>  
F;236-257/Domain: transmembrane #status predicted <TM6>  
F;285-300/Domain: transmembrane #status predicted <TM7>  
F;20-269,101-178/Disulfide bonds: #status predicted  
F;268/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;336,337,342/Binding site: phosphate (Ser) (covalent) #status predicted  
F;340,343/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 71.8%; Score 1364; DB 2; Length 352;  
Best Local Similarity 75.5%; Pred. No. 1.6e-108;  
Matches 259; Conservative 32; Mismatches 46; Indels 6; Gaps 2;

QY 24 FDYDY--GAPCHKFDVYKQIGAOQLPPLYSLVIFGFGVGNMLVLLINCKKLCITDYL 81  
Db 10 YDINYTSEPCQKLNKQJAARLLPPLYSLVIFGFGVGNMLVLLINCKKLSMTDYL 69  
QY 82 LNLASDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGVFGGFIILLTIDRYLA 141  
Db 70 LNLASDLLFLITLPLWAHSAANEWVFGNAMCKLFTGLYHIGVFGGFIILLTIDRYLA 129  
QY 142 IVHAFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVVCGPYPP---RG 197  
Db 130 VVHAFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVVCGPYPP---RG 189  
QY 198 WNNFHTIMRNILGLVPLLMVCIYSGILKTLRCRNEKRRHRAVRVIFIMIVYFLFW 257  
Db 190 WKNFHTIMRNILGLVPLLMVCIYSGILKTLRCRNEKRRHRAVRVIFIMIVYFLFW 249  
QY 258 PYNIVILLNTFQFFGLSNCESTSQLDAQVTTGLMTHCCINPIIYAFVGEKFRYLS 317  
Db 250 PYNIVILLNTFQFFGLSNCESTSQLDAQVTTGLMTHCCINPIIYAFVGEKFRYLS 309  
QY 318 VFERKHTKRCPCVYFRETVDGVTSTNTPSPGGEVSAGL 360  
Db 310 VFERKHTKRCPCVYFRETVDGVTSTNTPSPGGEVSAGL 352

RESULT 4  
A45177  
chemokine (C-C) receptor 1 - human  
N;Alternate names: C-C CR-1; macrophage inflammatory protein-1-alpha receptor  
C;Species: Homo sapiens (man)  
C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 13-Aug-1999  
C;Accession: A45177; I55671  
R;Neote, K.; DiGregorio, D.; Mak, J.Y.; Horuk, R.; Schall, T.J.  
Cell 72, 415-425, 1993  
A;Title: Molecular cloning, functional expression, and signaling characteristics of a C-  
cell chemokine receptor, human MIP-1 alpha  
A;Reference number: A45177; MUID:93161416; PMID:7679328  
A;Accession: A45177  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-355 <NEO>  
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417  
A;Experimental source: HL60 cells  
A;Note: sequence extracted from NCBI backbone (NCBIP:124876)  
R;Gao, J.  
J. Exp. Med. 177, 1421-1427, 1993  
A;Title: Structure and functional expression of the human macrophage inflammatory 1 alpha  
A;Reference number: I55671; MUID:93240122; PMID:7683036  
A;Accession: I55671  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-355 <RES>  
A;Cross-references: GB:L10918; NID:g292416; PIDN:AAA36543.1; PID:g292417  
C;Genetics:  
A;Gene: GDB:CMKBR1; CMKR-1  
A;Cross-references: GDB:138446; OMIM:601159  
A;Map position: 3p21-3p22  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: disulfide bond; G protein-coupled receptor; glycoprotein; phosphoprotein; tr

F;36-60/Domain: transmembrane #status predicted <TM1>  
F;71-91/Domain: transmembrane #status predicted <TM2>  
F;108-129/Domain: transmembrane #status predicted <TM3>  
F;147-171/Domain: transmembrane #status predicted <TM4>  
F;205-223/Domain: transmembrane #status predicted <TM5>  
F;240-264/Domain: transmembrane #status predicted <TM6>  
F;288-305/Domain: transmembrane #status predicted <TM7>  
F;5/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;24-273,106-183/Disulfide bonds: #status predicted  
F;345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 54.5%; Score 1036; DB 2; Length 355;  
Best Local Similarity 56.4%; Pred. No. 1.2e-80;  
Matches 199; Conservative 56; Mismatches 90; Indels 8; Gaps 5;

QY 12 NTNSESSEVTFDFDYCAPCHKFDVYKQIGAOQLPPLYSLVIFGFGVGNMLVLLINCK 71  
Db 5 NTTED-VDTTFDFDYCAPCHKFDVYKQIGAOQLPPLYSLVIFGFGVGNMLVLLINCK 63  
QY 72 KKLCTDIYLLNLAISSDLLFLITLPLWA-HSAANEWVFGNAMCKLFTGLYHIGVFGGFI 130  
Db 64 RLKNTSIYLLNLAISSDLLFLITLPLWFIDYKLDKDDWFGDAMCKLISGFIYTGISEIFF 123  
QY 131 IILITIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVVVC 190  
Db 124 IILITIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVVVC 183  
QY 191 GPYP---RGNNFHTIMRNILGLVPLLMVCIYSGILKTLRCRNEKRRHRAVRVIF 246  
Db 184 SLHPSHESLREMKLQALKNLGLVPLLMVCIYSGILKTLRCRNEKRRHRAVRVIF 242  
QY 247 TIMVYFLFWPYNIVILLNTFQFFGLSNCESTSQLDAQVTTGLMTHCCINPIIYA 306  
Db 243 VIMIIFLFWPYNIVILLNTFQFFGLSNCESTSQLDAQVTTGLMTHCCINPIIYA 302  
QY 307 FVGEKFRYLSVFFRKHTKRCPCVYFRETVDGVTSTNTPSPGGEVSAG 359  
Db 303 FVGEKFRYLSVFFRKHTKRCPCVYFRETVDGVTSTNTPSPGGEVSAG 354

RESULT 5  
I49341  
MIP-1 alpha receptor like-2 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 02-Jul-1998  
C;Accession: I49341  
R;Gao, J.L.; Murphy, P.M.  
J. Biol. Chem. 270, 17494-17501, 1995  
A;Title: Cloning and differential tissue-specific expression of three mouse beta chemokine  
receptor-like-2 (MIP-1-like-2) cDNAs  
A;Reference number: I49341; MUID:95340546; PMID:7542241  
A;Accession: I49341  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-359 <RES>  
A;Cross-references: EMBL:U28406; NID:g881551; PID:g881552  
C;Superfamily: vertebrate rhodopsin

Query Match 53.2%; Score 1010.5; DB 2; Length 359;  
Best Local Similarity 53.5%; Pred. No. 1.9e-78;  
Matches 193; Conservative 62; Mismatches 81; Indels 25; Gaps 6;

QY 10 IRNTNESSEVTFDFDYCAPCHKFDVYKQIGAOQLPPLYSLVIFGFGVGNMLVLLIN 69  
Db 8 IKTVVESE--TTPYEWEAPCEKVRKELGSLWLLPPLYSLVIFGFGVGNMLVLLIN 65  
QY 70 CKKLKCLFDIYLLNLAISSDLLFLITLPLWAHSA-NEWVFGNAMCKLFTGLYHIGVFGGI 128  
Db 66 YRKLQIMTNIYLLNLAISSDLLFLITLPLWFVFIWVHVLNNEWFGHGMCKMLSGFYLLALYSEI 125  
QY 129 FFIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVY 188  
Db 126 FFIILLTIDRYLAIVHAFALKARTVTFGVVTSVITWLVAVFASVPGIITKCKEDSVY 185

QY 189 VCGPFPFG-----WNNFHTIMRNILGLVPLLLIMVICYSIGILKTLRCRNEKKRHRAVRV 244  
 DB 186 SCSPRYPEGEEDSWKRFHRLMNFGLALPLLVWVICYSIGIILKTLRCPN-KKKHKAIRL 244  
 QY 245 IFTIMVYFLWTPYNYVILLNTFQEFFGLSNCESSTOLDQATQVETLGMTCCINPIL 304  
 DB 245 IFTIMVYFLWTPYNYVILLNTFQEFFGLSNCESSTOLDQATQVETLGMTCCINPIL 304  
 QY 305 YAFVGEKFRYLSVFRKHKRCKQCPVYRETV-----DGVTSNTSTPSTGQEV 356  
 DB 305 YAFVGEKFRYLSVFRKHKRCKQCPVYRETV-----DGVTSNTSTPSTGQEV 356  
 QY 357 S 357  
 DB 356 S 356

## RESULT 6

I49339

chemokine inflammatory protein-1 alpha receptor - mouse

Species: Mus musculus (house mouse)

Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 13-Aug-1999

C:Accession: I49339

R:Gao, J.L.; Murphy, P.M.

J. Biol. Chem. 270, 17494-17501, 1995

A:Title: Cloning and differential tissue-specific expression of three mouse beta chemokine

A:Reference number: I49339; MUID:95340546; PMID:7542241

A:Accession: I49339

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-355 &lt;RES&gt;

A:Cross-references: EMBL:U28404; NID:g881547; PIDN:AAA89153.1; PID:g8801548

C:Superfamily: vertebrate rhodopsin

Query Match 50.7%; Score 963.5; DB 2; Length 355;  
 Best Local Similarity 52.3%; Pred. No. 1.8e-74;  
 Matches 181; Conservative 65; Mismatches 89; Indels 11; Gaps 5;

QY 21 TTFEDYDYGACPKFEDVKQIGAOQLPPLYSILVIFGFGVGNMLVLLINCKKLCITDIY 80  
 DB 13 TTFEDYDYGACPKFEDVKQIGAOQLPPLYSILVIFGFGVGNMLVLLINCKKLCITDIY 80  
 QY 81 LLNLAISDLLFLITLPLWAHSA-ANEWVFGNAMCKLFTGLYHIGYFGGFIITLLIDRY 139  
 DB 73 LENLAVSLVFLFTPLFWIDYKLDKDWIFGDAMCKLLSGYILGLYSEIFFIILLIDRY 132  
 QY 140 LAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVVYVCGPYFP--- 195  
 DB 133 LAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVVYVCGPYFP--- 195  
 QY 196 RCWNNFHTIMRNILGLVPLLLIMVICYSIGILKTLRCRNEKKRHRAVRVIFTIMVYFLF 255  
 DB 193 KQWRFQALKNLGLLPLLVIMICYAGIIRLLR-RESEKKVAVRIFAITLLFLL 251  
 QY 256 WTPYNYVILLNTFQEFFGLSNCESSTOLDQATQVETLGMTCCINPILYAFVGEKFRY 315  
 DB 252 WTPYNYVILLNTFQEFFGLSNCESSTOLDQATQVETLGMTCCINPILYAFVGEKFRY 315  
 QY 316 LSVFPRKHITRCKQCPVYRETVGV---TSTNTPSTGQEVSA 359  
 DB 312 LRQFQRHVAIPALAKWLPFL---SVDQLERTSSISPSTGHELSAG 354

## RESULT 7

G02436

chemokine (C-C) receptor 3 - human

N:Alternate names: C-C CKR-3

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence\_revision 06-Jun-1997 #text\_change 04-Mar-2000

C:Accession: G02436; A57237

R:Ponath, P.D.

submitted to the EMBL Data Library, February 1996

A:Reference number: H01272

A:Accession: G02436

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-355 &lt;PON&gt;

A:Cross-references: EMBL:U49727; NID:gl477560; PIDN:AAB09726.1; PID:gl477561

R:Combadiere, C.; Ahuja, S.K.; Murphy, P.M.

J. Biol. Chem. 270, 16491-16494, 1995

A:Title: Cloning and functional expression of a human eosinophil CC chemokine receptor

A:Reference number: A57237; MUID:95348056; PMID:7622448

A:Accession: A57237

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-106,'N',108-275,'S',277-280,'R',282-355 &lt;COM&gt;

A:Cross-references: GB:U28694; NID:gl1199579; PIDN:AAC50469.1; PID:gl1199580

A:Note: the translated sequence in GenBank entry HSU28694, release 113.0, PIDN:AAC504

C:Genetics:

A:Gene: GDB:CMKBR3

A:Cross-references: GDB:579624; OMIM:601268

A:Map position: 3p21-3p21

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane

F:36-60/Domain: transmembrane #status predicted &lt;TM1&gt;

F:71-91/Domain: transmembrane #status predicted &lt;TM2&gt;

F:108-129/Domain: transmembrane #status predicted &lt;TM3&gt;

F:147-171/Domain: transmembrane #status predicted &lt;TM4&gt;

F:205-223/Domain: transmembrane #status predicted &lt;TM5&gt;

F:240-261/Domain: transmembrane #status predicted &lt;TM6&gt;

F:288-305/Domain: transmembrane #status predicted &lt;TM7&gt;

F:24-273,106-183/Disulfide bonds: #status predicted

F:345/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predicted

Query Match 50.1%; Score 951; DB 2; Length 355;  
 Best Local Similarity 52.6%; Pred. No. 2.1e-73;  
 Matches 180; Conservative 65; Mismatches 89; Indels 8; Gaps 5;

QY 21 TTFEDYDYGACPKFEDVKQIGAOQLPPLYSILVIFGFGVGNMLVLLINCKKLCITDIY 80  
 DB 14 TSYID-DVGLCEKADRALMAQFPPLYSILVFTVGLGNVWVVMILIKYRLRIMTY 72  
 QY 81 LLNLAISDLLFLITLPLWAHSA-ANEWVFGNAMCKLFTGLYHIGYFGGFIITLLIDRY 139  
 DB 73 LLNLAISDLLFLITLPLFWIHYVRGHNWVFGHGMCKLLSGFYHTGLYSEIFFIILLIDRY 132  
 QY 140 LAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVVYVCGPYFP--- 196  
 DB 133 LAIVHAFALKARTVTFGVTSVITWLVAVFASVPGIIFTKCKEDSVVYVCGPYFP--- 196  
 QY 197 -GWNNFHTIMRNILGLVPLLLIMVICYSIGILKTLRCRNEKKRHRAVRVIFTIMVYFLF 255  
 DB 193 YSWRHFHTLRTIFCLVPLLVMAICYTGILKLRCPFS-KKKYKAILRILFVMAVFFIF 251  
 QY 256 WTPYNYVILLNTFQEFFGLSNCESSTOLDQATQVETLGMTCCINPILYAFVGEKFRY 315  
 DB 252 WTPYNYVILLNTFQEFFGLSNCESSTOLDQATQVETLGMTCCINPILYAFVGEKFRY 315  
 QY 316 LSVFPRKHITRCKQCPVYRETVGVTSNTPSTGQEV 357  
 DB 312 LRHFFHRLHMLGRYIFPLPSEKLER-TSSVSPSTAEPELS 352

## RESULT 8

JC4587

chemokine (C-C) receptor 4 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 08-Mar-1996 #sequence\_revision 19-Apr-1996 #text\_change 20-Jun-2000

C:Accession: JC4587

R:Hoogwerf, A.J.; Black, D.; Proudfoot, A.E.I.; Wells, T.N.C.; Power, C.A.

Biochem. Biophys. Res. Commun. 218, 337-343, 1996

A:Title: Molecular cloning of murine CC CKR-4 and high affinity binding of chemokines

A:Reference number: JC4587; MUID:96136324; PMID:8573157

A:Accession: JC4587

A:Molecule type: mRNA

A:Residues: 1-360 &lt;HOO&gt;

A:Cross-references: EMBL:X90862; NID:g1167851; PIDN:CAA62372.1; PID:g1167852  
A:Experimental source: thymus  
C:Genetics:

A:Gene: cc ckr-4  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: glycoprotein; phosphoprotein; receptor; thymus  
F:2,183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:72,202,350/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted  
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted  
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 45.8%; Score 871; DB 2; Length 360;  
Best Local Similarity 47.5%; Pred. No. 1.4e-66;  
Matches 168; Conservative 71; Mismatches 103; Indels 12; Gaps 5;

QY 10 IRNTNESGEVTFEDYD-YGAPCHKFDVKQGAQLLPPLYSILVIFGVGNMLVLLILI 68  
Db 6 VTDITQDETIVNSYFESMPKPKCTKEGKAFGEVFLPPLYSILVIFLGLFGNSVVLVLF 65

QY 69 NCKLKCLDTIYLLNLALSDDLFLTLPLWAHSAANEVFGNAMCKLFTGLYHIGYEGGI 128  
Db 66 KYRKLKSWTDVYLLNLALSDDLFLVLSLFPWGYAADOVWFGGLCKIVSWMLVGVYSGI 125

QY 129 FFIILLTIDRYLAIVHAFVFAKARTVFGVVTSTVITWLVAVFASVPGIIFTRCKOKEDSVY 188  
Db 126 FFIMLSIDRYLAIVHAFVFAKARTVFGVVTSTVITWLVAVFASVPGIIFTRCKOKEDSVY 185

QY 189 VCGPYF---PRGWNFTIMRNILGLVPLIMVTCYSGILKTLRCRNEKRRHRAVRI 245  
Db 186 YCKTQSYNSNTWKVLSLEINVLGLLPLGIMLFWSMIIRTLQCKNEKK-NRAVRMI 244

QY 246 FTIMVVFVFWTPYTNIVILLNTFOFFGLSNCESTSQLDOATQVETLGMTHCCINPIY 305  
Db 245 FGVVVLGLFWTPNIVLLNTFOFFGLSNCESTSQLDOATQVETLGMTHCCINPIY 304

QY 306 AFVGEKFRYLSVFFRKHITKR---FCQKCPVYFRETVDGVTSTNTPTSTGEQE 355  
Db 305 FFLGEKFRKYITQLFR---TCRGPVLCKHCDFLQVYSDMSSSYTQSTVDHD 355

RESULT 9  
A57160  
chemokine (C-C) receptor 4 - human  
N:Alternate names: C-C CKR-4  
C:Species: Homo sapiens (man)  
C:Date: 10-Nov-1995 #sequence\_revision 10-Nov-1995 #text\_change 21-Jul-2000  
C:Accession: A57160  
R:Power, C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.; W  
J. Biol. Chem. 270, 19495-19500, 1995  
A:Title: Molecular cloning and functional expression of a novel CC chemokine receptor c  
A:Reference number: A57160; MUID:95370289; PMID:7642634  
A:Accession: A57160  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-360 <POW>  
A:Cross-references: GB:X85740; NID:g1370103; PIDN:CAA59743.1; PID:g971452  
A:Note: source clone K5-5  
C:Genetics:

A:Cross-references: GDB:677463  
A:Map position: 3p21-3p21  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot  
F:40-65/Domain: transmembrane #status predicted <TM1>  
F:76-97/Domain: transmembrane #status predicted <TM2>  
F:112-133/Domain: transmembrane #status predicted <TM3>  
F:151-175/Domain: transmembrane #status predicted <TM4>  
F:208-226/Domain: transmembrane #status predicted <TM5>  
F:243-264/Domain: transmembrane #status predicted <TM6>  
F:291-308/Domain: transmembrane #status predicted <TM7>  
F:29-276,110-187/disulfide bonds: #status predicted  
F:72,350/Binding site: phosphate (Ser) (covalent) (by protein kinase II) #status predicted  
F:145/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted

F:183,194/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match 45.4%; Score 862.5; DB 2; Length 360;  
Best Local Similarity 48.7%; Pred. No. 7.2e-66;  
Matches 164; Conservative 67; Mismatches 95; Indels 11; Gaps 4;

QY 31 PCHEFDVKQGAQLLPPLYSILVIFGVGNMLVLLINCKKLKCLTDIYLLNLALSDDL 90  
Db 28 PCKEGIKRAGEFLPPLYSILVIFGVGNMLVLLINCKKLKCLTDIYLLNLALSDDL 87

QY 91 FLITPLWAHSAANEVFGNAMCKLFTGLYHIGYEGGIFFIILLTIDRYLAIVHAFVFAK 150  
Db 88 FVPSLPGWGYAADOVWFGGLCKMISWMLVGVSGIIFVFMMSIDRYLAIVHAFVSLR 147

QY 151 ARTVTFGVVTSTVITWLVAVFASVPGIIFTRCKOKEDSVYVCGPYFPRG---WNNFTIMRN 207  
Db 148 ARTLYGVITSLATWSAVFASVPGIIFTRCKOKEDSVYVCGPYFPRG---WNNFTIMRN 207

QY 208 ILGLVPLIMVTCYSGILKTLRCRNEKRRHRAVRIFTIMVVFVFWTPYTNIVLLNT 267  
Db 208 ILGLVPLIMVTCYSGILKTLRCRNEKRRHRAVRIFTIMVVFVFWTPYTNIVLLNT 266

QY 268 FQEFFGLSNCESTSQLDOATQVETLGMTHCCINPIYAFVGEKFRYLSVFFRKHITKR 327  
Db 267 LVELEVLDQCTFERYLDYAIQATETLAFVHCCLNPIYFFLGEKFRKYIQLQFK---TCR 323

QY 328 ----FCQKCPVYFRETVDGVTSTNTPTSTGEQEVSAAGL 360  
Db 324 GLFVLCQVGLLQIYSADTPSSSYTQSTMDHDLHAL 360

RESULT 10  
S55594  
G protein-coupled receptor E1 - equine herpesvirus 2  
C:Species: equine herpesvirus 2  
C:Date: 10-Apr-1996 #sequence\_revision 19-Apr-1996 #text\_change 13-Aug-1999  
C:Accession: S55594  
R:Teiford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.  
J. Mol. Biol. 249, 520-528, 1995  
A:Title: The DNA sequence of equine herpesvirus 2.  
A:Reference number: S55594; MUID:95302501; PMID:7783207  
A:Accession: S55594  
A:Status: preliminary; nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-383 <TEL>  
A:Cross-references: GB:U20824; NID:g695172; PIDN:AAC13788.1; PID:g695173  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor

Query Match 43.3%; Score 822.5; DB 2; Length 383;  
Best Local Similarity 47.9%; Pred. No. 1.9e-62;  
Matches 162; Conservative 60; Mismatches 107; Indels 9; Gaps 4;

QY 4 TSRSRFRTRNTNESCSEEVTFEDYD-CAPCHKFDVKQGAQLLPPLYSILVIFGVGNM 61  
Db 32 TTTASLVPSNTSSSEYDDDDVDVEESAPCYKSTTRIAAQVVPALYLLVFLGLLGN 91

QY 62 LVVLILINCKKLKCLTDIYLLNLALSDDLFLTLPLWAH---SAAANEVFGNAMCKLFTGL 119  
Db 92 LVVIIVIRYMKIKKLTNMLLNALSDDLFLTLPLFWMHYIGMYHDWTFGSLCKLLRGV 151

QY 120 YHIGYFGGIFIIILLTIDRYLAIVHAFVFAKARTVFGVVTSTVITWLVAVFASVGIIFT 179  
Db 152 CYMSLSYQVFCIILLTVDYLVAVYATLFRFTVTCGIVTCVCTWFLAGLSLSEFFPH 211

QY 180 KCKEDSVYVCGPYF---RGWNNFTIMRNILGLVPLIMVTCYSGILKTLRCRNE 235  
Db 212 GHODNGRVQCDPYPEPMSTNWRRAHVAKVIMLSLILPLLMVAVYVIRRLUR-RPS 270

QY 236 KKRHRAVRVIFTIMVVFVFWTPYTNIVLLNTFOFFGLSNCESTSQLDOATQVETLGM 295  
Db 271 KKKYKARLIFVINVAVFVFWTPYTNIVLLNTFFHATLNLQCALSSNLDMLLITKTAVY 330



Search completed: May 19, 2003, 16:49:16  
Job time : 28.9564 secs

